

[illegible]

Db	1141	GGTTTGACCAATCGCAAAAGCCATGGCTGGGACCGTGTGAGCTGCTTGCAAAAGCGCTCG	1200
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Qy	2221	acgtgacccgtgaaaggttcgcgcttcaataaacctttagtttccaagaatcttcacatg	2280

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 11:23:48 ; Search time 73.57 Seconds
(without alignments)
8229.332 Million cell updates/sec

Title: US-08-956-991-1

Perfect score: 6604

Sequence: 1 tgactgagcgccgagcagcgcg.....gaaatgcgaatatatc 6604

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database : Issued Patents_NA:*

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- 3: /cgn2_6/ptodata/2/ina/5C.COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/5D.COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCITUS.CtIP.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	66.4	1.0	6000	2	US-08-348-006B-6	Sequence 6, Appli
2	66.4	1.0	6000	4	US-08-800-825A-6	Sequence 6, Appli
3	66.4	1.0	6000	5	PCT-US94-10165-6	Sequence 6, Appli
4	62.2	0.9	801	4	US-08-770-379-15	Sequence 16, Appli
5	62	0.9	12001	3	US-08-458-568A-11	Sequence 11, Appli
6	62	0.9	4257	4	US-08-690-473-1	Sequence 11, Appli
7	61.5	0.9	4403	4	US-08-284-941-1	Sequence 1, Appli
8	61.6	0.9	4403	5	PCT-US93-02147A-1	Sequence 1, Appli
9	60.4	0.9	8438	1	US-07-945-283-1	Sequence 1, Appli
10	60.2	0.9	1026	1	US-07-975-526-6	Sequence 1, Appli
11	59.4	0.9	12001	3	US-08-458-568A-11	Sequence 6, Appli
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13	58.8	0.9	44377	4	US-08-804-227C-7	Sequence 7, Appli
14	56.6	0.9	2823	2	US-08-398-008A-1	Sequence 1, Appli
15	55.6	0.8	43280	4	US-08-804-227C-1	Sequence 1, Appli
16	55.4	0.8	1610	1	US-08-056-051-5	Sequence 5, Appli
17	55.4	0.8	803	1	US-07-928-611-12	Sequence 12, Appli
18	55.4	0.8	1610	1	US-07-928-611-12	Sequence 21, Appli
19	55.4	0.8	803	4	US-08-487-811A-12	Sequence 12, Appli
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22	55.4	0.8	1610	5	PCT-US93-07370-12	Sequence 21, Appli
23	55.2	0.8	5117	5	PCT-US95-05512-1	Sequence 1, Appli
24	55	0.8	936	2	US-08-018-977C-4	Sequence 12, Appli
25	54.2	0.8	5467	1	US-07-745-206A-12	Sequence 7, Appli
26	54.2	0.8	7362	3	US-08-455-543A-8	Sequence 8, Appli
27	54.2	0.8	7175	3	US-08-455-543A-8	Sequence 17, Appli
28	54.2	0.8	1550	4	US-08-609-443B-17	Sequence 8, Appli
29	54.2	0.8	7362	4	US-08-193-078B-7	Sequence 8, Appli
30	54.2	0.8	7175	4	US-08-193-078B-7	Sequence 8, Appli
31	54.2	0.8	7362	4	US-08-223-305C-8	Sequence 8, Appli
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33	54.2	0.8	7362	4	US-08-149-097D-7	Sequence 8, Appli
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35	54.2	0.8	5467	4	US-08-311-363-12	Sequence 14, Appli
36	53.8	0.8	6453	3	US-08-305-691B-14	Sequence 3, Appli
37	53.4	0.8	2483	2	US-08-464-340A-3	Sequence 3, Appli

C 38	53.4	0.8	2483	5	PCT-US94-08449A-3	Sequence 3, Appli
C 39	53.2	0.8	1335	5	PCT-US91-06532-1	Sequence 1, Appli
C 40	53	0.8	6407	4	US-08-516-844-7	Sequence 7, Appli
C 41	53	0.8	6407	4	US-08-599-654-7	Sequence 7, Appli
42	52.6	0.8	936	2	US-08-018-977C-4	Sequence 4, Appli
43	52.6	0.8	7011	3	US-08-305-691B-42	Sequence 42, Appli
44	52.6	0.8	4524	4	US-08-845-998-7	Sequence 7, Appli
C 45	52.4	0.8	2003	1	US-08-036-555B-21	Sequence 21, Appli

ALIGNMENTS

```
RESULT 1
US-08-348-006B-6
: Sequence 6, Application US/08348006B
: Patent No. 5658756
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A.
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASE
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: J. MARK HAND
: STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
: CITY: RAHWAY
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/348,006B
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/122,032
: FILING DATE: 14-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: HAND, J., MARK
: REGISTRATION NUMBER: 35,745
: REFERENCE/DOCKET NUMBER: 189721A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-594-4905
: TELEFAX: 908-594-4720
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6000 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-348-006B-6

Query Match 1.0%; Score 66.4; DB 2; Length 6000;
Best Local Similarity 47.7%; Pred. No. 7.5e-07;
Matches 22; Conservative 0; Mismatches 246; Indels 3; Gaps 1:

QY 3597 tacacccctgacacactgaatgaatcaatcaatcagtcgcttggtgcaagcctgtaac 3656
||| ||||| ||||| ||| ||||| ||| |||||
Db 1721 TACGTGTGTGAGAGACCTGAGACCCCAACAGGAGTACGCTTCGCGCGGCCCTG 1780
||| ||||| ||||| ||| ||||| ||| |||||
QY 3657 cggcgccgagcggcgctcttcttcaggaatcatcaccacacacttcgaggaatgtgcc 3716
||| ||||| ||||| ||| ||||| ||| |||||
Db 1781 CCGGAGGGGCTTGGCGGCTTTCACACCCCGGTGGCGGCGGCGGCGGCTGCAATCAACCG 1840
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QY 3717 agtaccgcccccgaatatgtccaaagcatagcaatcaaccgcgaagaagcatatcatatcc 3776
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match Length DB ID Description
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1	6212	94.1	6413	11	AF023450	AF023450 Homo sapi
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5	699	10.6	721	11	HUMZ291FE03	AF086100 Homo sapi
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19	296	4.5	159424	12	AF064865	AF064865 Homo sapi
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21	78	1.2	331519	18	CEY39B6	Z95399 Caenorhabdit
22	75.8	1.1	3252	11	HSTAR1113	Y11354 H.sapiens r
23	75.8	1.1	3252	12	HSTAR1113	Y11354 H.sapiens r
24	74.8	1.1	135301	17	BHYIGEN	AJ004401 Bovine her
25	74.8	1.1	8113	17	HSBB1CP4A	L14320 Bovine herp
26	73.4	1.1	43054	11	HSBG1	284721 Human DNA s
27	73.4	1.1	2665	11	HUMHBA3	J00184 Human alpha
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29	73.4	1.1	2665	12	HUMHBA3	J00184 Human alpha
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31	72	1.1	38939	11	AC004678	AC004678 Homo sapi
32	72	1.1	38939	12	AC004678	AC004678 Homo sapi
33	72	1.1	38939	42	AC004678	AC004678 Homo sapi
34	71.8	1.1	2065	5	GG474726	U47272 Gallus gall
35	71.6	1.1	2764	17	HSBB1CP4B	L14321 Bovine herp
36	70.4	1.1	73	11	HSZ98234	Z98234 H.sapiens l
37	70.4	1.1	73	11	HSZ98234	Z98234 H.sapiens l
38	69.6	1.1	3957	6	A45258	A45258 Sequence 2
39	69.6	1.1	154746	17	HSV2HG52	Z86099 Herpes simp
40	68.8	1.0	1560	17	HSV2IE	M29384 Herpes simp
41	68.2	1.0	42301	12	AC005943	AC005943 Homo sapi
42	68.2	1.0	42301	13	AC005943	AC005943 Homo sapi
43	67.8	1.0	1839	5	S46000	S46000 TGF beta 3-
44	67.8	1.0	10144	10	HUMHMGIT	L17131 Human high
45	67.8	1.0	4233	12	H5U75308	U75308 Human TBF-

ALIGNMENTS

RESULT	1
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LOCUS	
DEFINITION	AF023450 6413 bp mRNA PRI 02-JUN-1998
ACCESSION	nrna, complete cds.
NID	AF023450
KEYWORDS	g3159767
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. .
REFERENCE	1 (bases 1 to 6413)
AUTHORS	Iamkawa,K., Huo,Y.-K., Haendel,M.A., Hubert,R., Chen,X.-N., Lyons,G.E. and Korenberg,J.R. DSCAM: A Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System
TITLE	unpublished
JOURNAL	2 (bases 1 to 6413).
REFERENCE	Iamkawa,K., Huo,Y.-K., Haendel,M.A., Hubert,R., Chen,X.-N., Lyons,G.E. and Korenberg,J.R. Direct Submission
AUTHORS	
TITLE	

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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 09:42:16 ; Search time 795.19 Seconds
(without alignments)
12688.348 Million cell updates/sec

Title: US-08-956-991-1

Perfect score: 6604
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Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database:

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2: em_est2:*
3: em_est3:*
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39: qb_est20:*
40: qb_est21:*
41: qb_est22:*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	374.2	5.7	510	13	N80326	N80326 y291f03.r1
C 4	358.8	5.4	430	12	N64532	N64532 y291f03.s1
C 5	343.8	5.2	355	34	HS1003472	A1003472 H.sapiens
C 6	318	4.8	321	13	HSC2WH042	Z11519 H.sapiens
C 7	303.4	4.6	307	39	A1051251	A1051251 oy49e04.x
C 8	288	4.4	310	12	HSC2XA021	F13426 H.sapiens
C 9	278	4.2	294	13	HSC2WH041	Z45894 H.sapiens
C 10	254.8	3.9	337	15	AA170935	AA170935 ms45h05.r
C 11	242.4	3.7	252	12	HSC2XA022	F09100 H.sapiens
C 12	187	2.8	187	36	AA878733	AA878733 oe80d01.s
C 13	187	1.9	646	41	A1106884	A1106884 GR06134.5
C 14	113.4	1.7	298	17	AA325603	AA325603 EST28915
C 15	90.6	1.4	786	41	AA697364	AA697364 HL02328.5
C 16	77.6	1.2	1056	13	W42205	W42205 mc69e09.r1
C 17	73.8	1.1	759	13	W28277	W28277 44q8 Human
C 18	73.2	1.1	1257	13	W98479	W98479 mg20c12.r1
C 19	73	1.1	1049	13	W42199	W42199 mc69c09.r1
C 20	72	1.1	1070	14	W29531	W29531 mc03g12.r1
C 21	71.8	1.1	1161	13	W41959	W41959 mc68b10.r1
C 22	70.8	1.1	1145	14	W29156	W29156 mb96a09.r1
C 23	70.4	1.1	1162	13	W42215	W42215 mc69h10.r1
C 24	70.2	1.1	1311	14	W15735	W15735 mb53g03.r1
C 25	70.2	1.1	459	41	A1285778	A1285778 qu56b02.x
C 26	69.8	1.1	1145	14	AA028476	AA028476 m121e10.r
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C 28	68.6	1.0	413	41	A1249175	A1249175 qh68904.x
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C 30	67.4	1.0	1137	14	W29428	W29428 mb96g03.r1
C 31	67.4	1.0	363	41	AA697625	AA697625 HL02894.5
C 32	66.2	1.0	1461	14	W15723	W15723 mb53c01.r1
C 33	66.2	1.0	1208	14	W29297	W29297 mb99e03.r1
C 34	66	1.0	1084	15	AA028875	AA028875 mh90d12.r
C 35	65.6	1.0	830	13	W28827	W28827 52c5 Human
C 36	65.4	1.0	1243	13	W42204	W42204 mc69g11.r1
C 37	65.4	1.0	424	41	A1270350	A1270350 qu86g12.x
C 38	64.8	1.0	859	13	W28841	W28841 52d7 Human
C 39	64.6	1.0	1044	13	W42217	W42217 mc69h12.r1
C 40	64.4	1.0	1100	15	AA203745	AA203745 zx53f05.r
C 41	64.2	1.0	763	13	W25843	W25843 13h6 Human
C 42	64.2	1.0	407	40	A1250825	A1250825 gx04f05.x
C 43	63.4	1.0	1111	13	W41963	W41963 mc68d10.r1
C 44	63.4	1.0	1286	13	W42216	W42216 mc69h11.r1
C 45	63	1.0	1068	14	W29367	W29367 mc03h09.r1

ALIGNMENTS

RESULT 1
A1243628/c
LOCUS qN88a03.x1 Source: NPL-T-GNC.S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1654028 3', mRNA sequence.
ACCESSION A1243628
NID q3839025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 439)
AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
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IMAGE Consortium (info@image.nih.gov) for further information.
Insert Length: 476 Std Error: 0.00
Seq primer: -40UP from Gibco.


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1 MetrPILLeuAlaLeuSerLeuPheGlnSerPheAlaAsnValPheSe 17
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17 rGluAspLeuHisSerSerLeuTyrPheValAsnAlaSerLeuGlnIuV 34
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503 TGAAGCCTTACACTCCAGCTTACTTCTCTCATCATCTCTCGCAAGAG 552
34 aValAlaPheAlaSerThrThrGlyThrLeuValProCysProAlaAlaGly 50
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553 TAGTGTTCCTCAGACACGCGGAGCTGTGTCCTCGCCCGCACAGAGC 602
51 lIleProProValThrLeuArgTyrThrLeuAlaThrGlyGluIleTy 67
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603 ATCCCTCTCTGTGACTCTCAGATGTGACTAGCCACGCGGAGAGAGATCTA 652
67 rAspValProGlyIleArgHisValHisProAsnGlyThrLeuGlnIleP 84
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653 CGATGTCCCGGGATCCGCGAGTCCACCCCAACGCGCACTCTCCAAATT 702
84 heProheProProSerSerPheSerThrLeuIleHisAsnThrTyr 100
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703 TCCCTTCCCTCTCTCAGAGCTTACAGCTTATCCATGA AATACTTAT 752
101 TyrCysThrAlaGluAsnProSerGlyLysIleArgSerGlnAspValH 117
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753 TATTGCACAGCTCAAAATCCTTCAGGAAATAGAAAGTCAGATGTCGA 802
117 sIleLysAlaValLeuArgGluProTyrThrValArgValGluAspGln 134
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151 ValGluAlaTyrIleThrValValSerTrpGluLysAspThrValSerLe 167
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903 GTGGAGGCTATACATCACTGCTCTCTCATGGAGAAAGACACTGTTTCACT 952
167 uValSerGlySerArgPheLeuIleThrSerThrGlyAlaLeuTyrIle 184
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953 TGCTCAGGATCTAGATTTCATCATCATCATCCAGCGAGCCTTGATATTA 1002
184 yAspValGlnAsnGluAspGlyLeuTyrAsnTyrArgCysIleThrArg 200
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1003 AAGATGTACACAATGAAGATGATTGATAACTACCGTCGATCAGCGCG 1052
201 HisArgTyrThrGlyGluThrArgGlnSerAsnSerAlaArgLeuPheVa 217
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1053 CATCATTCACCGCGAGAGACGAGCAGAGCAACAGCGCGCACTTTTGT 1102
217 lSerAspProAlaAsnSerAlaProSerIleLeuAspGlyPheAspHisA 234
|||||
1103 ATCAACACCAGAGACTCAGCCCATCATCTGATGGTTGACCATC 1152
234 rGlyAlaMetAlaGlyGlnArgValGluLeuProCysLysAlaLeuGly 250
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1153 GCAAGCCATGGCTGGCAGCGGTGGAGCTGCCCTTCGAAAGCGCTCGGG 1202
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[illegible]